

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/882,431A

INPUT SET: S31372.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

RECEIVED

APR 28 2000

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4 (i) APPLICANT: Robert G. Ulrich,
5 Mark A. Olson
6 Sina Bavari
7
8 (ii) TITLE OF INVENTION: Bacterial Superantigen
9 Vaccines
10
11 (iii) NUMBER OF SEQUENCES:16
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Charles H. Harris
15 (B) STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
16 (C) CITY: FORT DETRICK
17 (D) STATE: MARYLAND
18 (E) COUNTRY: USA
19 (F) ZIP: 21702-5012
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: Apple Macintosh
24 (C) OPERATING SYSTEM: Macintosh 7.5
25 (D) SOFTWARE: Microsoft Word 6.0
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 08/882,431
29 (B) FILING DATE: June 25, 1997
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER:
34 (B) FILING DATE:
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Charles H. Harris
38 (B) REGISTRATION NUMBER: 34,616
39 (C) REFERENCE/DOCKET NUMBER:
40
41 (ix) TELECOMMUNICATION INFORMATION
42 (A) TELEPHONE: (301) 619-2065
43 (B) TELEFAX: (301) 619-7714
44
45
46 (2) INFORMATION FOR SEQ ID NO:1:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/882,431ADATE: 04/09/1999
TIME: 19:23:51

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47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 830

49 (B) TYPE: Nucleic Acid

50 (C) STRANDEDNESS: Unknown

51 (D) TOPOLOGY: Unknown

52

53 (ii) MOLECULE TYPE: DNA

54

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

56

57 atgaaaaaaaa cagcatttac attactttta ttcattgccc 40

58

59 taacgttgac aacaagtcca cttgtaaatg gtagcgagaa 80

60

61 aagcgaagaa ataaatgaaa aagatttgcg aaaaaagtct 120

62

63 gaattgcagg gaacagcttt aggcaatctt aaacaaatct 160

64

65 attattacaa tgaaaaagct aaaactgaaa ataaagagag 200

66

67 tcacgatcaa tttcgacagc atactatatt gtttaaaggc 240

68

69 ttttttacag atcattcgtg gtataacgat ttattagtag 280

70

71 gttttgattc aaaggatatt gttgataaat ataaagggaa 320

72

73 aaaagtagac ttgtatggtg cttatgctgg ttatcaatgt 360

74

75 gcgggtggtg caccaaaca aacagcttgt atgtatggtg 400

76

77 gtgtaacgtt acatgataat aatcgattga ccgaagagaa 440

78

79 aaaagtgccg atcaatttat ggctagacgg taaacaaaat 480

80

81 acagtacctt tggaacggt taaaacgaat aagaaaaatg 520

82

83 taactgttca ggagttggat cttcaagcaa gacgttattt 560

84

85 acaggaaaaa tataatttat ataactctga tgtttttgat 600

86

87 gggaagggtc agaggggatt aatcgtgttt catacttcta 640

88

89 cagaaccttc ggttaattac gatttatttg gtgctcaagg 680

90

91 acagtattca aatacactat taagaatata tagagataat 720

92

93 aaaacgatta actctgaaaa catgcatatt gatatatatt 760

94

95 tatatacaag ttaaACATGG TAGTTTGGAC CAACGTAATG 800

96

97 TTCAGATTAT TATGAACCGA GAATAATCTA 830

98

99

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100 (2) INFORMATION FOR SEQ ID NO:2:
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 257
103 (B) TYPE: Amino Acid
104 (C) STRANDEDNESS: Unknown
105 (D) TOPOLOGY: Unknown
106 (ii) MOLECULE TYPE: Peptide
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
108
109 Met Lys Lys Thr Ala Phe Thr Leu Leu Leu
110 1 5 10
111
112 Phe Ile Ala Leu Thr Leu Thr Thr Ser Pro
113 15 20
114
115 Leu Val Asn Gly Ser Glu Lys Ser Glu Glu
116 25 30
117
118 Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
119 35 40
120
121 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu
122 45 50
123
124 Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala
125 55 60
126
127 Lys Thr Glu Asn Lys Glu Ser His Asp Gln
128 65 70
129
130 Phe Arg Gln His Thr Ile Leu Phe Lys Gly
131 75 80
132
133 Phe Phe Thr Asp His Ser Trp Tyr Asn Asp
134 85 90
135
136 Leu Leu Val Arg Phe Asp Ser Lys Asp Ile
137 95 100
138
139 Val Asp Lys Tyr Lys Gly Lys Lys Val Asp
140 105 110
141
142 Leu Tyr Gly Ala Tyr Ala Gly Tyr Gln Cys
143 115 120
144
145 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys
146 125 130
147
148 Met Tyr Gly Gly Val Thr Leu His Asp Asn
149 135 140
150
151 Asn Arg Leu Thr Glu Glu Lys Lys Val Pro
152 145 150

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153
154   Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
155                               155          160
156
157   Thr Val Pro Leu Glu Thr Val Lys Thr Asn
158                               165          170
159
160   Lys Lys Asn Val Thr Val Gln Glu Leu Asp
161                               175          180
162
163   Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys
164                               185          190
165
166   Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
167                               195          200
168
169   Gly Lys Val Gln Arg Gly Leu Ile Val Phe
170                               205          210
171
172   His Thr Ser Thr Glu Pro Ser Val Asn Tyr
173                               215          220
174
175   Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser
176                               225          230
177
178   Asn Thr Leu leu Arg Ile Tyr Arg Asp Asn
179                               235          240
180
181   Lys Thr Ile Asn Ser Glu Asn Met His Ile
182                               245          250
183
184   Asp Ile Tyr Leu Tyr Thr Ser
185                               255
186
187
188   (2) INFORMATION FOR SEQ ID NO:3:
189   (i) SEQUENCE CHARACTERISTICS:
190   (A) LENGTH: 757
191   (B) TYPE: Nucleic Acid
192   (C) STRANDEDNESS: Unknown
193   (D) TOPOLOGY: Unknown
194   (ii) MOLECULE TYPE: DNA
195
196   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
197
198   atgagaaaag cgaagaaata aatgaaaaag atttgcgaaa      40
199
200   aaagtctgaa ttgcagggaa cagctttagg caatcttaaa      80
201
202   Caaatctatt attacaatga aaaagctaaa actgaaaata      120
203
204   aagagagtca cgatcaattt cgacagcata ctatattgtt      160
205

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206   taaaggcttt tttacagatc attcgtggta taacgattta   200
207
208   ttagtacgtt ttgattcaaa ggatattgtt gataaatata   240
209
210   aagggaaaaa agtagacttg tatggtgctt atgctgggta   280
211
212   tcaatgtgcg ggtggtacac caaacaaaac agcttgatg   320
213
214   tatggtgggtg taacgttaca tgataataat cgattgaccg   360
215
216   aagagaaaaa agtgccgatc aatttatggc tagacggtaa   400
217
218   acaaaataca gtaccttggg aaacgggtaa aacgaataag   440
219
220   aaaaatgtaa ctgttcagga gttggatctt caagcaagac   480
221
222   gttatttaca ggaaaaatat aatttatata actctgatgt   520
223
224   ttttgatggg aaggttcaga ggggattaat cgtgtttcat   560
225
226   acttctacag aaccttcggt taattacgat ttatttggtg   600
227
228   ctcaaggaca gtattcaaat acactattaa gaatatatag   640
229
230   agataataaa acgattaact ctgaaaacat gcatattgat   680
231
232   atatatttat atacaagtta aACATGGTAG TTTTGACCAA   720
233
234   CGTAATGTTC AGATTATTAT GAACCGAGAA TAATCTA   757
235
236
237   (2) INFORMATION FOR SEQ ID NO:4:
238   (i) SEQUENCE CHARACTERISTICS:
239   (A) LENGTH:233
240   (B) TYPE: Amino Acid
241   (C) STRANDEDNESS: Unknown
242   (D) TOPOLOGY: Unknown
243   (ii) MOLECULE TYPE: Peptide
244   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
245
246   Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
247           5                               10
248
249   Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly
250           15                               20
25

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PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text